

T. Strzelecka

Re-run

21

6/24/03



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/689,992A

DATE: 06/23/2003

TIME: 16:03:44

Input Set : N:\paola\US09689992A.raw.txt

Output Set: N:\CRF4\06232003\I689992A.raw

C--> 1 <110> APPLICANT: Mello, Craig C.
2 Tabara, Hiroaki
3 Grishok, Alla
4 Fire, Andrew
5 <120> TITLE OF INVENTION: RNA INTERFERENCE PATHWAY GENES AS TOOLS FOR TARGETED GENETIC
6 INTERFERENCE
7 <130> FILE REFERENCE: UMG-052
8 <140> CURRENT APPLICATION NUMBER: US/09/689,992A
9 <141> CURRENT FILING DATE: 2000-10-13
10 <150> PRIOR APPLICATION NUMBER: US 60/193,218
11 <151> PRIOR FILING DATE: 2000-03-30
12 <150> PRIOR APPLICATION NUMBER: US 60/159,776
13 <151> PRIOR FILING DATE: 1999-10-15
14 <160> NUMBER OF SEQ ID NOS: 14
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 3719
19 <212> TYPE: DNA
20 <213> ORGANISM: Caenorhabditis elegans
21 <400> SEQUENCE: 1
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23 gtcattctct cgatccggtg tgatcaatta ttagcagcta taagatatat aagtttgata 120
24 ttaatattat aggagatgaa atggccttgcg aggcccaactg gtaaatgcca cggcaaattc 180
25 tatgagaaga aagtacttct tttggtaaaat tggttcaagt tctccagcaa aatttacgat 240
26 cggaataact acgagtatga agtgaaaatg acaaaggaag tattgaatag aaaaccagga 300
27 aaacctttcc caaaaaagac agaaaattcca atgtaagtgc ttgtaaaatta gtcaaaacta 360
28 attttatttt tcagtcccgga tcgtgcaaaa ctcttctggc aacatcttcg gcatgagaag 420
29 aagcagacag attttattct cgaagactat gtttttgatg aaaaggacac tgtttatagt 480
30 gtttgctcgac tgaacactgt cacatcaaaa atgctgggtt cggagaaaagt agtaaaaaag 540
31 gattcgggaga aaaaagatga aaaggatttg gagaaaaaaa tcttatacac aatgatactt 600
32 acctatcgta aaaaatttca cctgaacttt agtcgagaaa atccggaaaa agacgaagaa 660
33 gcgaatcgga gttacaaatt cctgaagggtt tatgaaaaac acgcattata acaaacaaaa 720
34 ttagctttca gaatgttatg acccagaaaag ttcgctacgc gccttttgatg aacgaggaga 780
35 ttaaagtgtg agttgcaata ataataataa taatcacctc aactcattta tatattttaa 840
36 gacaattcgc gaaaaatttt gtgtacgata ataattcaat tctgcgagtt cctgaatcgt 900
37 ttcacgatcc aaacagattc gaacaatcat tagaagtagc accaagaatc gaagcatggt 960
38 ttggaattta cattggaatc aaagaattgt tcgatgggtga acctgtgctc aattttgcaa 1020
39 gtaagtttga gaaactgcca taaaaaatca tgtgattttt gttgaagttg tcgataaaact 1080
40 attctacaat gcaccgaaaa tgtctcttct ggattatctt ctccctaattg tcgaccccca 1140
41 gtcgtgtaac gatgatgtac gaaaagatct taaaacaaaa ctgatggcgg gaaaaatgac 1200
42 aatcagacaa gccgcgcggc caagaattcg acaattattg gaaaatttga agctgaaatg 1260
43 cgcaagaagt tgggataacg aaatgttagt ttaaattatt caaacaatta atatacaaat 1320
44 tgattttcag gtcgagattg acagaacgac atctgacatt tctagatttg tgcgaggaaa 1380

ENTERED

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46 atactacatt gttcaaaatc tatgaggaaa acaaaaagtt cattgagttt cccacacctac 1500
47 cactagtcaa agttaaagtc ggagcaaaag aatacgctgt accaatggaa catcttgaag 1560
48 ttcattgagaa gccacaaaaga tacaagaatc gaattgatct ggtgatgcaa gacaagtttc 1620
49 taaagcgcgc tacacgaaaaa cctcacgact acaaagaaaa taccctaaaa atgctgaaaag 1680
50 aattggattt ctcttctgaa gagctaaatt ttgttgaaaag atttgattta tgctccaaac 1740
51 ttcagatgat cgaatgtcca ggaaaggttt tgaaagagcc aatgcttggtg aatagtgtaa 1800
52 atgaacaaat taaaatgaca ccagtgattc gtggatttca agaaaaacaa ttgaatgtgg 1860
53 ttcccgaaaa agaactttgc tgtgctgttt ttgtagtcaa cgaaacagcg ggaaatccat 1920
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56 aatgaaaaca gaggagcgca atctattatg tacgacgcga cgaaaaatga atatgccgta 2100
57 agtttcagaa aattgaaagt ttttaaatat catatttaca gttctacaaa aattgttacac 2160
58 taaataccgg aatcggtaga tttgaaatag ccgcaacaga agcgaagaat atgtttgaac 2220
59 gtcttcccga taaagaacaa aaagtcttaa tgttcattat catttccaaa cgacaactga 2280
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62 gaattttcta tcaaattgca ttgaaaatca acgcgaaatt aggaggtatt aaccaggagc 2460
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64 cattaactat gtatgttgga attgatgtaa ctcatccaac ctctacagt ggaattgatt 2580
65 attctatagc ggctgtagta gcgagtatca atccagggtg aactatctat cgaaatatga 2640
66 ttgtgactca agaagaatgt cgtcccgtg agcgtgcagt ggctcatgga cgggaaagaa 2700
67 cagatatttt ggaagcaaag ttcgtgaaat tgctcagaga attcgcagaa gtgagttgtc 2760
68 ttgagtattt aaaagatctc tgggattttt aatttttttg taaactttca gaacaacgac 2820
69 aatcgagcac cagcgcata ttagtcttat cgagacggag ttagcgattc ggagatgcta 2880
70 cgtgttagtc atgatgagct tcgatcttta aaaagcgaag taaaacaatt catgtcggaa 2940
71 cgggatggag aagatccaga gccgaagtac acgttcattg tgattcagaa aagacacaat 3000
72 acacgattgc ttcgaagaat ggaaaaagat aagccagtgg tcaataaaga tcttactcct 3060
73 gctgaaacgc atgtcgctgt tgctgctgtt aaacaatggg aggaggatat gaaagaaagc 3120
74 aaagaaaactg gaattgtgaa cccatcatcc ggaacaactg tggataaact tatcgtttcg 3180
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77 gttttgaata gcagtttagc atttttaggat tttgtaatcc gcatatagtt attataaaaa 3360
78 aatgtttcag aaaatgacct acggacttgc ttttctctct gctagatgtc gaaaacccat 3420
79 ctcgttgcct gttccggttc attatgctca tttatcatgt gaaaaagcga aagagcttta 3480
80 tcgaacttac aaggaacatt acatcggtga ctatgcacag ccacggactc gacacgaaat 3540
81 ggaacatttt ctccaaacta acgtgaagta ccctggaatg tcgttcgcat aacattttgc 3600
82 aaaagtgtcg cccgtttcaa tcaaattttt caattgtaga tattgtactt actttttttt 3660
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85 <210> SEQ ID NO: 2

86 <211> LENGTH: 3227

87 <212> TYPE: DNA

88 <213> ORGANISM: Caenorhabditis elegans

89 <220> FEATURE:

90 <221> NAME/KEY: CDS

91 <222> LOCATION: (21)...(3080)

92 <400> SEQUENCE: 2

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93 cagccacaaa gtgatgaaac atg tcc tcg aat ttt ccc gaa ttg gaa aaa gga 53
94 Met Ser Ser Asn Phe Pro Glu Leu Glu Lys Gly

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Input Set : N:\paola\US09689992A.raw.txt

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96	ttt tat cgt cat tct ctc gat ccg gag atg aaa tgg ctt gcg agg ccc							101
97	Phe Tyr Arg His Ser Leu Asp Pro Glu Met Lys Trp Leu Ala Arg Pro							
98		15		20		25		
99	act ggt aaa tgc gac ggc aaa ttc tat gag aag aaa gta ctt ctt ttg							149
100	Thr Gly Lys Cys Asp Gly Lys Phe Tyr Glu Lys Lys Val Leu Leu Leu							
101		30		35		40		
102	gta aat tgg ttc aag ttc tcc agc aaa att tac gat cgg gaa tac tac							197
103	Val Asn Trp Phe Lys Phe Ser Ser Lys Ile Tyr Asp Arg Glu Tyr Tyr							
104		45		50		55		
105	gag tat gaa gtg aaa atg aca aag gaa gta ttg aat aga aaa cca gga							245
106	Glu Tyr Glu Val Lys Met Thr Lys Glu Val Leu Asn Arg Lys Pro Gly							
107		60		65		70		75
108	aaa cct ttc cca aaa aag aca gaa att cca att ccc gat cgt gca aaa							293
109	Lys Pro Phe Pro Lys Lys Thr Glu Ile Pro Ile Pro Asp Arg Ala Lys							
110		80		85		90		
111	ctc ttc tgg caa cat ctt cgg cat gag aag aag cag aca gat ttt att							341
112	Leu Phe Trp Gln His Leu Arg His Glu Lys Lys Gln Thr Asp Phe Ile							
113		95		100		105		
114	ctc gaa gac tat gtt ttt gat gaa aag gac act gtt tat agt gtt tgt							389
115	Leu Glu Asp Tyr Val Phe Asp Glu Lys Asp Thr Val Tyr Ser Val Cys							
116		110		115		120		
117	cga ctg aac act gtc aca tca aaa atg ctg gtt tcg gag aaa gta gta							437
118	Arg Leu Asn Thr Val Thr Ser Lys Met Leu Val Ser Glu Lys Val Val							
119		125		130		135		
120	aaa aag gat tcg gag aaa aaa gat gaa aag gat ttg gag aaa aaa atc							485
121	Lys Lys Asp Ser Glu Lys Lys Asp Glu Lys Asp Leu Glu Lys Lys Ile							
122		140		145		150		155
123	tta tac aca atg ata ctt acc tat cgt aaa aaa ttt cac ctg aac ttt							533
124	Leu Tyr Thr Met Ile Leu Thr Tyr Arg Lys Lys Phe His Leu Asn Phe							
125		160		165		170		
126	agt cga gaa aat ccg gaa aaa gac gaa gaa gcg aat ccg agt tac aaa							581
127	Ser Arg Glu Asn Pro Glu Lys Asp Glu Glu Ala Asn Arg Ser Tyr Lys							
128		175		180		185		
129	ttc ctg aag aat gtt atg acc cag aaa gtt cgc tac gcg cct ttt gtg							629
130	Phe Leu Lys Asn Val Met Thr Gln Lys Val Arg Tyr Ala Pro Phe Val							
131		190		195		200		
132	aac gag gag att aaa gta caa ttc gcg aaa aat ttt gtg tac gat aat							677
133	Asn Glu Glu Ile Lys Val Gln Phe Ala Lys Asn Phe Val Tyr Asp Asn							
134		205		210		215		
135	aat tca att ctg cga gtt cct gaa tcg ttt cac gat cca aac aga ttc							725
136	Asn Ser Ile Leu Arg Val Pro Glu Ser Phe His Asp Pro Asn Arg Phe							
137		220		225		230		235
138	gaa caa tca tta gaa gta gca cca aga atc gaa gca tgg ttt gga att							773
139	Glu Gln Ser Leu Glu Val Ala Pro Arg Ile Glu Ala Trp Phe Gly Ile							
140		240		245		250		
141	tac att gga atc aaa gaa ttg ttc gat ggt gaa cct gtg ctc aat ttt							821
142	Tyr Ile Gly Ile Lys Glu Leu Phe Asp Gly Glu Pro Val Leu Asn Phe							
143		255		260		265		

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146	270 275 280	
147	gat tat ctt ctc cta att gtc gac ccc cag tcg tgt aac gat gat gta	917
148	Asp Tyr Leu Leu Leu Ile Val Asp Pro Gln Ser Cys Asn Asp Asp Val	
149	285 290 295	
150	cga aaa gat ctt aaa aca aaa ctg atg gcg gga aaa atg aca atc aga	965
151	Arg Lys Asp Leu Lys Thr Lys Leu Met Ala Gly Lys Met Thr Ile Arg	
152	300 305 310	
153	caa gcc gcg cgg cca aga att cga caa tta ttg gaa aat ttg aag ctg	1013
154	Gln Ala Ala Arg Pro Arg Ile Arg Gln Leu Glu Asn Leu Lys Leu	
155	320 325 330	
156	aaa tgc gca gaa gtt tgg gat aac gaa atg tcg aga ttg aca gaa cga	1061
157	Lys Cys Ala Glu Val Trp Asp Asn Glu Met Ser Arg Leu Thr Glu Arg	
158	335 340 345	
159	cat ctg aca ttt cta gat ttg tgc gag gaa aac tct ctt gtt tat aaa	1109
160	His Leu Thr Phe Leu Asp Leu Cys Glu Glu Asn Ser Leu Val Tyr Lys	
161	350 355 360	
162	gtc act ggt aaa tcg gac aga gga aga aat gca aaa aag tac gat act	1157
163	Val Thr Gly Lys Ser Asp Arg Gly Arg Asn Ala Lys Lys Tyr Asp Thr	
164	365 370 375	
165	aca ttg ttc aaa atc tat gag gaa aac aaa aag ttc att gag ttt ccc	1205
166	Thr Leu Phe Lys Ile Tyr Glu Glu Asn Lys Lys Phe Ile Glu Phe Pro	
167	380 385 390	
168	cac cta cca cta gtc aaa gtt aaa agt gga gca aaa gaa tac gct gta	1253
169	His Leu Pro Leu Val Lys Val Lys Ser Gly Ala Lys Glu Tyr Ala Val	
170	400 405 410	
171	cca atg gaa cat ctt gaa gtt cat gag aag cca caa aga tac aag aat	1301
172	Pro Met Glu His Leu Glu Val His Glu Lys Pro Gln Arg Tyr Lys Asn	
173	415 420 425	
174	cga att gat ctg gtg atg caa gac aag ttt cta aag cga gct aca cga	1349
175	Arg Ile Asp Leu Val Met Gln Asp Lys Phe Leu Lys Arg Ala Thr Arg	
176	430 435 440	
177	aaa cct cac gac tac aaa gaa aat acc cta aaa atg ctg aaa gaa ttg	1397
178	Lys Pro His Asp Tyr Lys Glu Asn Thr Leu Lys Met Leu Lys Glu Leu	
179	445 450 455	
180	gat ttc tct tct gaa gag cta aat ttt gtt gaa aga ttt gga tta tgc	1445
181	Asp Phe Ser Ser Glu Glu Leu Asn Phe Val Glu Arg Phe Gly Leu Cys	
182	460 465 470	
183	tcc aaa ctt cag atg atc gaa tgt cca gga aag gtt ttg aaa gag cca	1493
184	Ser Lys Leu Gln Met Ile Glu Cys Pro Gly Lys Val Leu Lys Glu Pro	
185	480 485 490	
186	atg ctt gtg aat agt gta aat gaa caa att aaa atg aca cca gtg att	1541
187	Met Leu Val Asn Ser Val Asn Glu Gln Ile Lys Met Thr Pro Val Ile	
188	495 500 505	
189	cgt gga ttt caa gaa aaa caa ttg aat gtg gtt ccc gaa aaa gaa ctt	1589
190	Arg Gly Phe Gln Glu Lys Gln Leu Asn Val Val Pro Glu Lys Glu Leu	
191	510 515 520	
192	tgc tgt gct gtt ttt gta gtc aac gaa aca gcg gga aat cca tgc tta	1637

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193	Cys	Cys	Ala	Val	Phe	Val	Val	Asn	Glu	Thr	Ala	Gly	Asn	Pro	Cys	Leu	
194		525					530					535					
195	gaa	gag	aac	gac	gtt	gtt	aag	ttc	tac	acc	gaa	cta	att	ggt	ggt	tgc	1685
196	Glu	Glu	Asn	Asp	Val	Val	Lys	Phe	Tyr	Thr	Glu	Leu	Ile	Gly	Gly	Cys	
197	540					545					550					555	
198	aag	ttc	cgt	gga	ata	cga	att	ggt	gcc	aat	gaa	aac	aga	gga	gcg	caa	1733
199	Lys	Phe	Arg	Gly	Ile	Arg	Ile	Gly	Ala	Asn	Glu	Asn	Arg	Gly	Ala	Gln	
200					560					565					570		
201	tct	att	atg	tac	gac	gcg	acg	aaa	aat	gaa	tat	gcc	ttc	tac	aaa	aat	1781
202	Ser	Ile	Met	Tyr	Asp	Ala	Thr	Lys	Asn	Glu	Tyr	Ala	Phe	Tyr	Lys	Asn	
203			575						580					585			
204	tgt	aca	cta	aat	acc	gga	atc	ggt	aga	ttt	gaa	ata	gcc	gca	aca	gaa	1829
205	Cys	Thr	Leu	Asn	Thr	Gly	Ile	Gly	Arg	Phe	Glu	Ile	Ala	Ala	Thr	Glu	
206			590					595					600				
207	gcg	aag	aat	atg	ttt	gaa	cgt	ctt	ccc	gat	aaa	gaa	caa	aaa	gtc	tta	1877
208	Ala	Lys	Asn	Met	Phe	Glu	Arg	Leu	Pro	Asp	Lys	Glu	Gln	Lys	Val	Leu	
209			605				610					615					
210	atg	ttc	att	atc	att	tcc	aaa	cga	caa	ctg	aat	gct	tac	ggt	ttt	gtg	1925
211	Met	Phe	Ile	Ile	Ile	Ser	Lys	Arg	Gln	Leu	Asn	Ala	Tyr	Gly	Phe	Val	
212	620					625					630					635	
213	aaa	cat	tat	tgc	gat	cac	acc	atc	ggt	gta	gct	aat	cag	cat	att	act	1973
214	Lys	His	Tyr	Cys	Asp	His	Thr	Ile	Gly	Val	Ala	Asn	Gln	His	Ile	Thr	
215					640					645					650		
216	tct	gaa	aca	gtc	aca	aaa	gct	ttg	gca	tca	cta	agg	cac	gag	aaa	gga	2021
217	Ser	Glu	Thr	Val	Thr	Lys	Ala	Leu	Ala	Ser	Leu	Arg	His	Glu	Lys	Gly	
218				655					660					665			
219	tca	aaa	cga	att	ttc	tat	caa	att	gca	ttg	aaa	atc	aac	gcg	aaa	tta	2069
220	Ser	Lys	Arg	Ile	Phe	Tyr	Gln	Ile	Ala	Leu	Lys	Ile	Asn	Ala	Lys	Leu	
221			670					675				680					
222	gga	ggt	att	aac	cag	gag	ctt	gac	tgg	tca	gaa	att	gca	gaa	ata	tca	2117
223	Gly	Gly	Ile	Asn	Gln	Glu	Leu	Asp	Trp	Ser	Glu	Ile	Ala	Glu	Ile	Ser	
224			685				690					695					
225	cca	gaa	gaa	aaa	gaa	aga	cgg	aaa	aca	atg	cca	tta	act	atg	tat	gtt	2165
226	Pro	Glu	Glu	Lys	Glu	Arg	Arg	Lys	Thr	Met	Pro	Leu	Thr	Met	Tyr	Val	
227	700					705					710					715	
228	gga	att	gat	gta	act	cat	cca	acc	tcc	tac	agt	gga	att	gat	tat	tct	2213
229	Gly	Ile	Asp	Val	Thr	His	Pro	Thr	Ser	Tyr	Ser	Gly	Ile	Asp	Tyr	Ser	
230					720					725					730		
231	ata	gcg	gct	gta	gta	gcg	agt	atc	aat	cca	ggt	gga	act	atc	tat	cga	2261
232	Ile	Ala	Ala	Val	Val	Ala	Ser	Ile	Asn	Pro	Gly	Gly	Thr	Ile	Tyr	Arg	
233				735					740					745			
234	aat	atg	att	gtg	act	caa	gaa	gaa	tgt	cgt	ccc	ggt	gag	cgt	gca	gtg	2309
235	Asn	Met	Ile	Val	Thr	Gln	Glu	Glu	Cys	Arg	Pro	Gly	Glu	Arg	Ala	Val	
236			750					755				760					
237	gct	cat	gga	cgg	gaa	aga	aca	gat	att	ttg	gaa	gca	aag	ttc	gtg	aaa	2357
238	Ala	His	Gly	Arg	Glu	Arg	Thr	Asp	Ile	Leu	Glu	Ala	Lys	Phe	Val	Lys	
239			765				770					775					
240	ttg	ctc	aga	gaa	ttc	gca	gaa	aac	aac	gac	aat	cga	gca	cca	gcg	cat	2405
241	Leu	Leu	Arg	Glu	Phe	Ala	Glu	Asn	Asn	Asp	Asn	Arg	Ala	Pro	Ala	His	

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 386,400,402

Seq#:8; Xaa Pos. 2,3,4,6,8,9,10,12,13,14,15,16,17,18,19,21,22,23,24,25,26

Seq#:8; Xaa Pos. 29,31,32,33,35,36,37,39,40,41,43,44,45,46,47,49,51,55,56

Seq#:8; Xaa Pos. 59,60,63,64,67,68

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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L:8 M:270 C: Current Application Number differs, Wrong Format
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:384
M:341 Repeated in SeqNo=5
L:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
M:341 Repeated in SeqNo=8